UNITED STATES PATENT AND TRADEMARK OFFICE

UNITED STATES DEPARTMENT OF COMMERCE
United States Patent and Trademark Office
Address: COMMISSIONER FOR PATENTS
P.O. Box 1450
Alexandria, Virginia 22313-1450
www.uspto.gov

APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
10/533,176	04/12/2006	Bret Cooper	1392/10/20 PCT/US	2356

25297 7590 04/04/2008

JENKINS, WILSON, TAYLOR & HUNT, P. A.
3100 TOWER BLVD., Suite 1200
DURHAM, NC 27707

EXAMINER	
COLLINS, CYNTHIA E	
ART UNIT	**PAPER NUMBER**
1638	
MAIL DATE	**DELIVERY MODE**
04/04/2008	PAPER

Please find below and/or attached an Office communication concerning this application or proceeding.

The time period for reply, if any, is set in the attached communication.

Office Action Summary	Application No.	Applicant(s)	
	10/533,176	COOPER, BRET	
	Examiner	Art Unit	
	Cynthia Collins	1638	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE *3* MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *14 January 2008*.

2a)☐ This action is **FINAL**. 2b)☒ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *1-46* is/are pending in the application.

4a) Of the above claim(s) *5-15,17,18 and 27-29* is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *1-4,16,19-26 and 30-46* is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☐ The specification is objected to by the Examiner.

10)☒ The drawing(s) filed on *29 April 2005* is/are: a)☐ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☒ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☒ Information Disclosure Statement(s) (PTO/SB/08) Paper No(s)/Mail Date *53105,6905,51806,91406,42307*.
4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____ .
5) ☐ Notice of Informal Patent Application
6) ☐ Other: _____.

DETAILED ACTION

Election/Restrictions

Applicant's election with traverse of Group I, claims 1-4, 16, 19-26 and 30-46, drawn to an isolated nucleic acid of SEQ ID NO:1, a transgenic plant or plant cell, an expression cassette, and methods of using said nucleic acid and expression cassette to transform plant cells, in the reply filed on January 14, 2008 is acknowledged.

The traversal is on the ground(s) that it would not constitute an undue search burden for the Patent Office to examine all of the claims of Groups I-VIII together. In particular, applicants respectfully submit that the polypeptides encoded by nucleic acids of SEQ ID NOs: 1, 3, 5, 7, 9, 11, 13 and 15, i.e. Groups I-VIII, each bind in a yeast two hybrid assay to a fragment of a protein of SEQ ID NO: 114, i.e. OsGF14-c, as recited in amended claims 1, 27 and 42. Applicants respectfully direct the Patent Office's attention to Table 1, at pages 133-135 of the specification as filed. Applicants respectfully submit that the ability of each of the polypeptides of SEQ ID NOs: 2, 4, 6, 8, 10, 12, 14 and 16 to bind to a fragment of a protein of SEQ ID NO: 114 in a yeast two hybrid assay illustrates that each of these "prey" proteins has a structural commonality. In particular, each of the "prey" proteins bind to amino acids 1-150 of the "bait" protein (SEQ ID NO: 114). See, e.g., the column labeled "Bait Coord" of Table 1. Therefore, each of the isolated nucleic acids of SEQ [D NOs: 1, 3, 5, 7, 9, 11, 13 and 15, which encode for polypeptides of SEQ ID NOs: 2, 4, 6, 8, 10, 12, 14 and 16, respectively, are believed to possess the structural/functional commonality of encoding proteins capable of binding to OsGF14-c. Applicants submit that based on this special technical feature it would not constitute an undue

search burden for the Patent Office to examine all of the claims of Groups J-VIII together. Accordingly, applicants respectfully request that Groups I-VIII be examined together.

This is not found persuasive because the commonality of encoding proteins capable of binding in a yeast two hybrid assay to a fragment of a protein consisting of OsGF14-c (SEQ ID NO: 114) recited in the pending claims does not constitute a special technical feature as defined by PCT Rule 13.2, because it does not define a contribution over the prior art, because it is obvious or anticipated over Schultz T.F. et al. (14-3-3 proteins are part of an abscisic acid-VIVIPAROUS1 (VP1) response complex in the Em promoter and interact with VP1 and EmBP1. Plant Cell. 1998 May;10(5):837-47). See also Applicant's specification page 135.

This is also not found persuasive because the commonality of encoding proteins capable of binding in a yeast two hybrid assay to a fragment of a protein consisting of OsGF14-c (SEQ ID NO: 114), is a functional commonality, not a structural (technical) commonality, of the claimed nucleic acid molecules. While these sequences share a common function, a shared substantial structural feature essential to that function, if it exists, is neither apparent nor disclosed. It is necessary that a shared substantial structural feature essential to the shared common function be apparent or disclosed because a complete search of the claimed subject matter requires a structural search. A structural search of the claimed subject matter is required because a known composition may have heretofore unrecognized functional characteristics. In the absence of an apparent or disclosed shared substantial structural feature essential to the shared common function, it would constitute an undue search burden for the Patent Office to examine all of the claims of Groups I-VIII together, because each individual sequence must be separately searched.

Accordingly, claims 5-15, 17-18 and 27-29, and the nonelected sequences, are withdrawn from consideration.

The requirement is still deemed proper and is therefore made FINAL.

Claim Objections

Claims 1-4, 16, 19-26 and 30-46 are objected to because they are directed in part to nonelected inventions. Appropriate correction is required.

Claim Rejections - 35 USC § 112

The following is a quotation of the first paragraph of 35 U.S.C. 112:

> The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

Claims 1-2, 16, 19-26, 30, 32-38 and 40-44 are rejected under 35 U.S.C. 112, first paragraph, as failing to comply with the written description requirement. The claim(s) contains subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention.

The claims are drawn to an isolated nucleic acid molecule encoding a stress-related polypeptide, wherein the polypeptide binds in a yeast two hybrid assay to a fragment of a protein of OsGF14-c (SEQ ID NO: 114), including an isolated nucleic acid molecule is derived from rice (Oryza sativa).

The claims are also drawn to an isolated nucleic acid molecule encoding a stress-related polypeptide, wherein the nucleic acid molecule has a nucleic acid sequence at least 90% identical to SEQ ID NO:1 or a nucleic acid encoding SEQ ID NO:2 or a nucleic acid that hybridizes to a nucleic acid molecule of SEQ ID NO:1 or encoding SEQ ID NO:2 under defined stringency conditions.

The claims are additionally drawn to a transgenic plant cell or plant and an expression cassette comprising an isolated nucleic acid molecules, and to methods that employ said expression cassette.

With respect to isolated nucleic acid molecules encoding a polypeptide wherein the polypeptide binds in a yeast two hybrid assay to a fragment of a protein of OsGF14-c (SEQ ID NO: 114), the specification describes 14 different types of such isolated nucleic acid molecules, including an isolated nucleic acid molecule having a nucleic acid sequence of SEQ ID NO:1 that encodes a polypeptide of SEQ ID NO:2 (pages 133-135 Table 1). While these sequences share a common function (encoding a polypeptide that binds in a yeast two hybrid assay to a fragment of a protein of OsGF14-c (SEQ ID NO: 114)), a shared substantial structural feature essential to that function, if it exists, is neither apparent nor disclosed.

With respect to isolated nucleic acid molecules encoding a polypeptide wherein the nucleic acid molecule has a nucleic acid sequence at least 90% identical to SEQ ID NO:1 or a nucleic acid encoding SEQ ID NO:2 or a nucleic acid that hybridizes to a nucleic acid molecule of SEQ ID NO:1 or encoding SEQ ID NO:2 under defined stringency conditions, the specification describes a single nucleic acid sequence of SEQ ID NO:1 that encodes a polypeptide of SEQ ID NO:2. The specification describes SEQ ID NO:1 as a 1383 bp

polynucleotide obtained from *Oryza sativa* that encodes a protein fragment (SEQ ID NO:2) designated as OsPN22858 and which is described as being similar to similar to *Arabidopsis thaliana* GTP cyclohydrolase II; 3,4-dihydroxy-2-butanone-4-phoshate synthase (GENBANK.RTM. Accession No. BAB09512.1, 74.4% identity, e=0), an enzyme which catalyzes the first committed reaction in the biosynthesis of the B vitamin riboflavin.

The specification does not disclose other nucleic acid sequences that are at least 90% identical to SEQ ID NO:1 or that hybridize to a nucleic acid molecule of SEQ ID NO:1 or encoding SEQ ID NO:2 under defined stringency conditions.

The Federal Circuit has clarified the application of the written description requirement to nucleic acid sequences. The court stated that "A description of a genus of cDNAs may be achieved by means of recitation of a representative number of cDNAs, defined by nucleotide sequence, falling within the scope of the genus or of a recitation of structural features common to members of the genus, which features constitute a substantial portion of the genus." See *University of California v. Eli Lilly and Co.*, 119 F.3d 1559, 1569; 43 USPQ2d 1398, 1406 (Fed. Cir. 1997). The court has also affirmed the PTO's applicable standard for determining compliance with the written description requirement, quoting from the PTO's Guidelines for Examination of Patent Applications Under the 35 U.S.C. 112, P1, "Written Description" Requirement, 66 Fed. Reg. 1099, 1106, where it is set forth that the written description requirement can be met by "show[ing] that an invention is complete by disclosure of sufficiently detailed, relevant identifying characteristics ... i.e., complete or partial structure, other physical and/or chemical properties, functional characteristics when coupled with a known or disclosed

correlation between function and structure, or some combination of such characteristics." See *Enzo Biochem Inc. v. Gen-Probe Inc.*, 63 USPQ2d 1609, 1613 (CAFC 2002).

In the instant case Applicant has not described a representative number of species falling within the scope of the claimed genus which encompasses numerous undisclosed and uncharacterized nucleic acid sequences that encode a polypeptide that binds in a yeast two hybrid assay to a fragment of a protein of OsGF14-c (SEQ ID NO: 114)., and which encompasses numerous undisclosed and uncharacterized nucleic acid sequences that are at least 90% identical to SEQ ID NO:1 or that hybridize to a nucleic acid molecule of SEQ ID NO:1 or encoding SEQ ID NO:2 under defined stringency conditions and that encode a polypeptide that binds in a yeast two hybrid assay to a fragment of a protein of OsGF14-c (SEQ ID NO: 114), nor the structural features unique to the genus that are correlated with encoding a polypeptide that binds in a yeast two hybrid assay to a fragment of a protein of OsGF14-c (SEQ ID NO: 114).

Claims 1-4, 16, 19-26 and 30-46 are rejected under 35 U.S.C. 112, first paragraph, as failing to comply with the enablement requirement. The claim(s) contains subject matter which was not described in the specification in such a way as to enable one skilled in the art to which it pertains, or with which it is most nearly connected, to make and/or use the invention.

The claims are drawn to an isolated nucleic acid molecule encoding a stress-related polypeptide, wherein the polypeptide binds in a yeast two hybrid assay to a fragment of a protein of OsGF14-c (SEQ ID NO: 114), including an isolated nucleic acid molecule is derived from rice (Oryza sativa).

The claims are also drawn to an isolated nucleic acid molecule encoding a stress-related polypeptide, wherein the nucleic acid molecule has a nucleic acid sequence at least 90% identical to SEQ ID NO:1 or a nucleic acid encoding SEQ ID NO:2 or a nucleic acid that hybridizes to a nucleic acid molecule of SEQ ID NO:1 or encoding SEQ ID NO:2 under defined stringency conditions.

The claims are additionally drawn to a transgenic plant cell or plant and an expression cassette comprising an isolated nucleic acid molecules, and to methods that employ said expression cassette.

The specification discloses that the *Oryza sativa* nucleic acid sequence of SEQ ID NO:1 encodes a polypeptide designated as OsPN22858 (SEQ ID NO:2) that binds in a yeast two hybrid assay to a fragment of an *Oryza sativa* 14-3-3 protein homolog designated as OsGF14-c (SEQ ID NO:114). The specification also discloses that OsPN22858 (SEQ ID NO:2) is a protein fragment that is structurally similar to *Arabidopsis thaliana* GTP cyclohydrolase II; 3,4-dihydroxy-2-butanone-4-phoshate synthase (GENBANK.RTM. Accession No. BAB09512.1, 74.4% identity, e=0), an enzyme which catalyzes the first committed reaction in the biosynthesis of the B vitamin riboflavin. (pages 133-134 Table 1; pp 137-147). The specification does not disclose any other specific function or activity for a nucleic acid sequence of SEQ ID NO:1 or for a nucleic acid sequence encoding a polypeptide of SEQ ID NO:2 or for a polypeptide of SEQ ID NO:2 . The specification also does not disclose other nucleic acid sequences that are at least 90% identical to SEQ ID NO:1 or that hybridize to a nucleic acid molecule of SEQ ID NO:1 or encoding SEQ ID NO:2 under defined stringency conditions. The specification additionally does not disclose the effect of expressing a nucleic acid sequence of SEQ ID NO:1 or a nucleic acid

sequence encoding a polypeptide of SEQ ID NO:2 or a polypeptide of SEQ ID NO:2 in a transgenic plant cell or plant.

The claimed invention is not enabled because the function of a sequence cannot reliably be predicted on the basis of its structure or its homology to other known sequences.

See, for example, Whisstock J.C. et al. (Prediction of protein function from protein sequence and structure. Q Rev Biophys. 2003 Aug;36(3):307-40. Review), who teach

> "... prediction of protein function from sequence and structure is a difficult problem, because homologous proteins often have different functions. Many methods of function prediction rely on identifying similarity in sequence and/or structure between a protein of unknown function and one or more well-understood proteins. Alternative methods include inferring conservation patterns in members of a functionally uncharacterized family for which many sequences and structures are known. However, these inferences are tenuous. Such methods provide reasonable guesses at function, but are far from foolproof." (Abstract)

Whisstock J.C. et al. also teach at page 309 that while the observation that similar sequences determine similar structures gives us general confidence in homology modeling, much less reliable is the widely held assumption that proteins with very similar sequences should by virtue of their very similar structures have similar functions. Whisstock J.C. et al. further teach at page 309 that to reason from sequence and structure to function is to step on much shakier ground, that while many families of proteins contain homologues with the same function, the assumption that homologues share function is less and less safe as the sequences progressively diverge, and that even closely related proteins can change function through divergence to a related function or by recruitment for as very different function in such cases the assignment of function on the basis of homology in the absence of direct experimental evidence will give the wrong answer.

Whisstock J.C. et al. additionally teach at page 310 that a protein need not even change sequence to change function, as numerous proteins exhibit multiple functions in different cellular environments such that even if detailed in vitro studies on isolated proteins do identity a function we cannot be sure we know the molecules full repertoire of biological activities, and that nonhomologous proteins may conversely have similar functions.

Whisstock J.C. et al. further teach that while general hints based on protein sequence, structure, genomics and interaction patterns may be useful in guiding experimental investigations of protein function,

> "inferring protein function from knowledge of the function of a close homologue is like solving the clue of an American crossword puzzle. Finding the word that satisfies the definition may be difficult but the task in principle is straightforward. Working out the function of a protein from its sequence and structure is like solving the clue of a British crossword puzzle. It is by no means obvious which features of the definition are providing the real clues, as opposed to misleading ones. Also, for both types of puzzle and for the suggestion of a protein function, even if your answer appears to fit it may be wrong." (pages 311-312).

The claimed invention is also not enabled because polypeptide function cannot be reliably predicted on the basis of a partial amino acid sequence, since polypeptides may require the presence of specific amino acid in order to function properly, which amino acids may not be present in a partial amino acid sequence.

See, for example, Kaiser J. et al. (Biosynthesis of vitamin B2. Eur J Biochem. 2002 Nov;269(21):5264-70), who analyzed the effect of the replacement of cysteine residue 54, 65 or 67 of GTP cyclohydrolase II with serine. While the mutant proteins retained the capacity to release pyrophosphate from GTP and from the formamide-type intermediate analog, replacement of cysteine residue 54, 65 or 67 with serine resulted in proteins devoid of bound zinc and unable

to release formate from the imidazole ring of GTP or from the intermediate analog, 2-amino-5-formylamino-6-ribosylamino-4(3H)-pyrimidinone 5'-triphosphate (abstract; page 5266 Table 3; 5267 Table 4 and Figure 4).

The claimed invention is additionally not enabled because the effect of expressing only part of a full-length polypeptide in transgenic plants is unpredictable.

See, for example, Zhou Y. et al. (The plant cyclin-dependent kinase inhibitor ICK1 has distinct functional domains for in vivo kinase inhibition, protein instability and nuclear localization.Plant J. 2003 Aug;35(4):476-89), who teach that expression of an N-terminal truncation of the *Arabidopsis* cyclin-dependent kinase inhibitor ICK1 increases ICK1 effects on transgenic plants, whereas expression of a C-terminal truncation of ICK1 greatly reduces or abolishes ICK1 effects on transgenic plants, as compared to control plants expressing the full-length ICK1 protein (page 476 Abstract; page 479 Figure 2; page 480 Table 1).

In the instant case the specification does not provide guidance with respect to how a nucleic acid sequence of SEQ ID NO:1 or encoding SEQ ID NO:2 may be used. Absent such guidance one skilled in the art would have to test and/or modify a nucleic acid sequence of SEQ ID NO:1 or encoding SEQ ID NO:2 in a variety of different undisclosed ways in order to identify a potential specific use for these sequences. The specification also does not provide guidance with respect to how a nucleic acid sequence of SEQ ID NO:1 or encoding SEQ ID NO:2 may be used to specifically alter a plant. Absent such guidance one skilled in the art would have to transform a variety of different types of plants with an expression cassette comprising a nucleic acid sequence of SEQ ID NO:1 or encoding SEQ ID NO:2, and then screen the plants for a variety of different phenotypic characteristics in order to identify a specific alternation that can

be produced by these sequences. Such a trial and error approach to practicing the claimed invention would constitute undue experimentation.

The following is a quotation of the second paragraph of 35 U.S.C. 112:

> The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

Claims 1, 16, 30, 31 and 42, and claims dependent thereon, are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention. Claims 1, 16, 30, 31 and 42 are indefinite in the recitation of "stress-related". It is unclear in what way the particular encoded polypeptide required by the claims is related to stress, because a polypeptide may be related to stress in a variety of different ways, and the relationship between the particular encoded polypeptide required by the claims and stress cannot be discerned from the claim limitations or from the disclosure.

Claim 42, and claims dependent thereon, are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention. Claim 42 is indefinite in the recitation of "modulating stress response of a plant cell". It is unclear in what type of stress response is modulated, or in what way the stress response is modulated, because plant cells exhibit numerous different types of responses to different types of stresses that can be modulated in a variety of different ways, and because the nature of the stress response modulated and the nature of the modulation cannot be discerned from the claim limitations or from the disclosure.

Claim 43 is rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention. Claim 43 is indefinite in the recitation of "enhancement", as "enhancement" is a relative term that lacks a comparative basis.

Claim 44 is rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention. Claim 44 is indefinite in the recitation of "decrease", as "decrease" is a relative term that lacks a comparative basis.

Claim Rejections - 35 USC § 101

35 U.S.C. 101 reads as follows:

> Whoever invents or discovers any new and useful process, machine, manufacture, or composition of matter, or any new and useful improvement thereof, may obtain a patent therefor, subject to the conditions and requirements of this title.

Claims 3, 4, 31, 39, 45 and 46 are rejected under 35 U.S.C. 101 because the claimed invention is not supported by either a specific and substantial asserted utility or a well established utility.

The claims are drawn to an isolated nucleic acid molecule encoding a stress-related polypeptide, wherein the nucleic acid molecule has a nucleic acid sequence of SEQ ID NO:1 or a nucleic acid encoding SEQ ID NO:2. The claims are also drawn to a transgenic plant cell or plant and an expression cassette comprising said isolated nucleic acid molecule, and to methods that employ said expression cassette.

The claimed invention is not supported by a well established utility because no use for SEQ ID NO:1 or its encoded polypeptide is taught in the prior art.

The claimed invention is not supported by a specific and substantial asserted utility because no specific and substantial use or function has been established for an isolated nucleic acid molecule of SEQ ID NO:1 encodes or its encoded polypeptide. While the specification discloses that an isolated nucleic acid molecule of SEQ ID NO:1 encodes a polypeptide that specifically binds in a yeast two hybrid assay to a fragment of a protein of OsGF14-c (SEQ ID NO: 114), such a utility is not substantial, because there is no disclosed or real world utility associated with this interaction, or with the claimed isolated nucleic acid molecule or with its encoded polypeptide. Further experimentation is therefore necessary to attribute a utility to the claimed invention. *See Brenner v. Manson*, 383 U.S. 519, 535–36, 148 USPQ 689, 696 (1966) (noting that "Congress intended that no patent be granted on a chemical compound whose sole "utility" consists of its potential role as an object of use-testing", and stated, in context of the utility requirement, that "a patent is not a hunting license. It is not a reward for the search, but compensation for its successful conclusion."). Additionally, since Applicant has not disclosed any specific and substantial utility for the claimed invention, credibility will not be assessed.

Claims 3, 4, 31, 39, 45 and 46 are also rejected under 35 U.S.C. 112, first paragraph. Specifically, since the claimed invention is not supported by either a specific and substantial asserted utility or a well established utility for the reasons set forth above, one skilled in the art clearly would not know how to use the claimed invention.

Claim Rejections - 35 USC § 102

The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

A person shall be entitled to a patent unless –

(b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.

(e) the invention was described in (1) an application for patent, published under section 122(b), by another filed in the United States before the invention by the applicant for patent or (2) a patent granted on an application for patent by another filed in the United States before the invention by the applicant for patent, except that an international application filed under the treaty defined in section 351(a) shall have the effects for purposes of this subsection of an application filed in the United States only if the international application designated the United States and was published under Article 21(2) of such treaty in the English language.

Claims 1-4 and 16 are rejected under 35 U.S.C. 102(e) as being anticipated by Allen et al. (US Patent No. 6,677,502, filed July 12, 2000 and issued January 13, 2004).

The claims are drawn a nucleic acid molecule comprising a nucleic acid sequence of SEQ ID NO:1.

Allen et al. teach a nucleic acid molecule comprising a nucleic acid sequence of SEQ ID NO:1 (SEQ ID NO:69 of Allen et al., see attached sequence alignment). The nucleic acid taught by Allen et al. inherently has the same functional attributes as the claimed nucleic acid molecules, because a nucleic acid's structure determines its functional attributes, and the structures are identical.

Claims 1, 19-20, 30-38 and 40-42 are rejected under 35 U.S.C. 102(b) as being anticipated by Suzuki M. et al. (Maize VP1 complements *Arabidopsis* abi3 and confers a novel ABA/auxin interaction in roots. Plant J. 2001 Nov;28(4):409-18).

The claims are drawn to an isolated nucleic acid molecule encoding a stress-related polypeptide, wherein the polypeptide binds in a yeast two hybrid assay to a fragment of a protein of OsGF14-c (SEQ ID NO: 114).

The claims are additionally drawn to a transgenic plant cell or plant or seeds or progeny and an expression cassette comprising said isolated nucleic acid molecule, including an expression cassette that

further comprises a regulatory element operativety linked to the nucleic acid molecule including a regulatory element that comprises a promoter including a plant promoter, a constitutive promoter, a tissue- specific or a cell type-specific promoter that directs expression of the expression cassette in a location selected from the group consisting of epidermis, root, vascular tissue, meristem, cambium, cortex, pith, leaf, flower, seed, and combinations thereof, and to methods that employ said expression cassette to transform plant cells.

Suzuki M. et al. teach an isolated nucleic acid molecule encoding a maize VP1 polypeptide (paragraph spanning pages 416-417). The maize VP1 polypeptide binds in a yeast two hybrid assay to a fragment of a protein of OsGF14-c (SEQ ID NO: 114) (Applicant's specification page 135). The maize VP1 polypeptide is a stress-related polypeptide because the mutation of the gene encoding maize VP1 causes loss of desiccation tolerance (page 409 column 1). Suzuki M. et al. also teach an expression cassette comprising said isolated nucleic acid molecule, including an expression cassette that further comprises a CaMV 35S promoter (paragraph spanning pages 416-417). The CaMV 35S promoter is a plant promoter because it function in plants, is a constitutive promoter because it has been so called in the prior art, is a tissue- specific or a cell type-specific promoter because it is known in the prior art to preferentially direct expression in a specific tissue or cell under certain circumstances and directs expression of the expression cassette in root (e.g. page 415 column 2). Suzuki M. et al. further teach the use of said expression cassette to transform plant cells and plant cells, plants and seeds or progeny thereof (page 410 Table 1; page 411 Figure 1; pages 416-417).

Remarks

No claim is allowed.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Cynthia Collins whose telephone number is (571) 272-0794. The examiner can normally be reached on Monday-Friday 8:45 AM -5:15 PM.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Anne Marie Grunberg can be reached on (571) 272-0975. The fax phone number for the organization where this application or proceeding is assigned is 571-273-8300.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see http://pair-direct.uspto.gov. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free). If you would like assistance from a USPTO Customer Service Representative or access to the automated information system, call 800-786-9199 (IN USA OR CANADA) or 571-272-1000.

/Cynthia Collins/
Primary Examiner, Art Unit 1638

CC